

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:13:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238277.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6238277 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238277.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:13:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238277.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,461,617
Mapped reads	1,082,575 / 74.07%
Unmapped reads	379,042 / 25.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,945 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	158,304 / 10.83%
Duplication rate	10.69%
Clipped reads	615,968 / 42.14%

2.2. ACGT Content

Number/percentage of A's	19,130,946 / 27.65%
Number/percentage of C's	13,276,286 / 19.19%
Number/percentage of T's	21,262,646 / 30.74%
Number/percentage of G's	15,493,568 / 22.4%
Number/percentage of N's	14,554 / 0.02%
GC Percentage	41.59%

2.3. Coverage

Mean	0.0224

Standard Deviation	0.3142
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2.4. Mapping Quality

Mean Mapping Quality	45.03
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2.5. Mismatches and indels

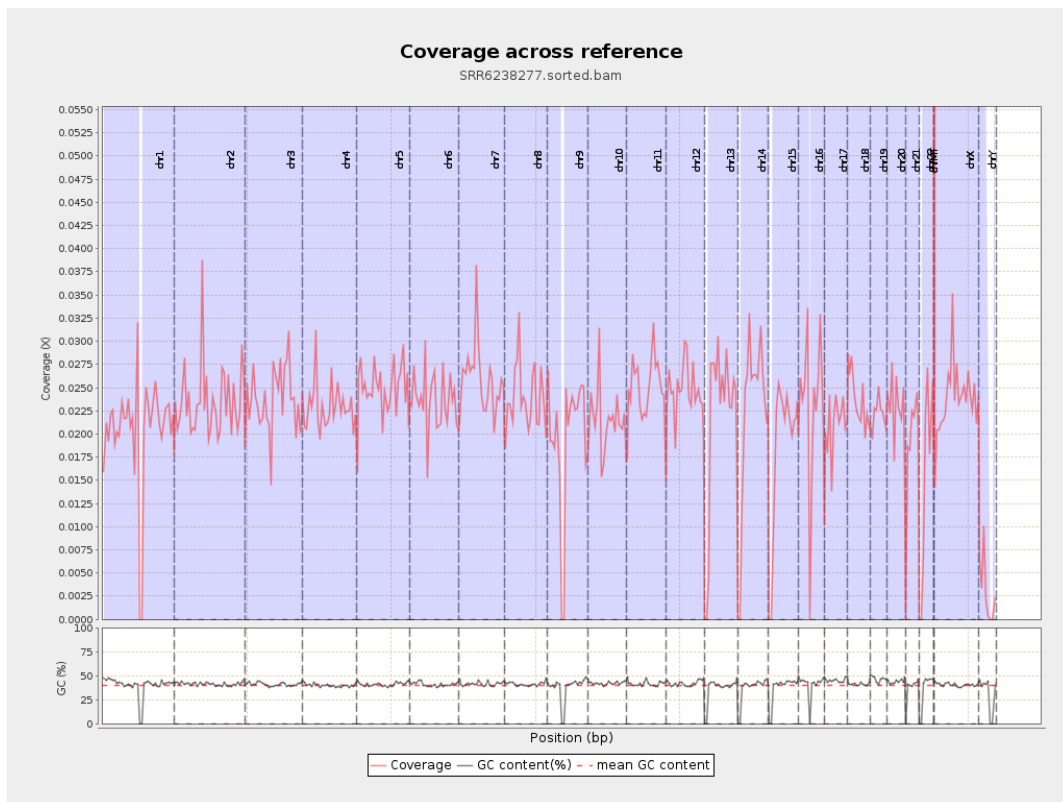
General error rate	0.96%
Mismatches	652,022
Insertions	5,604
Mapped reads with at least one insertion	0.51%
Deletions	23,107
Mapped reads with at least one deletion	2.11%
Homopolymer indels	46.99%

2.6. Chromosome stats

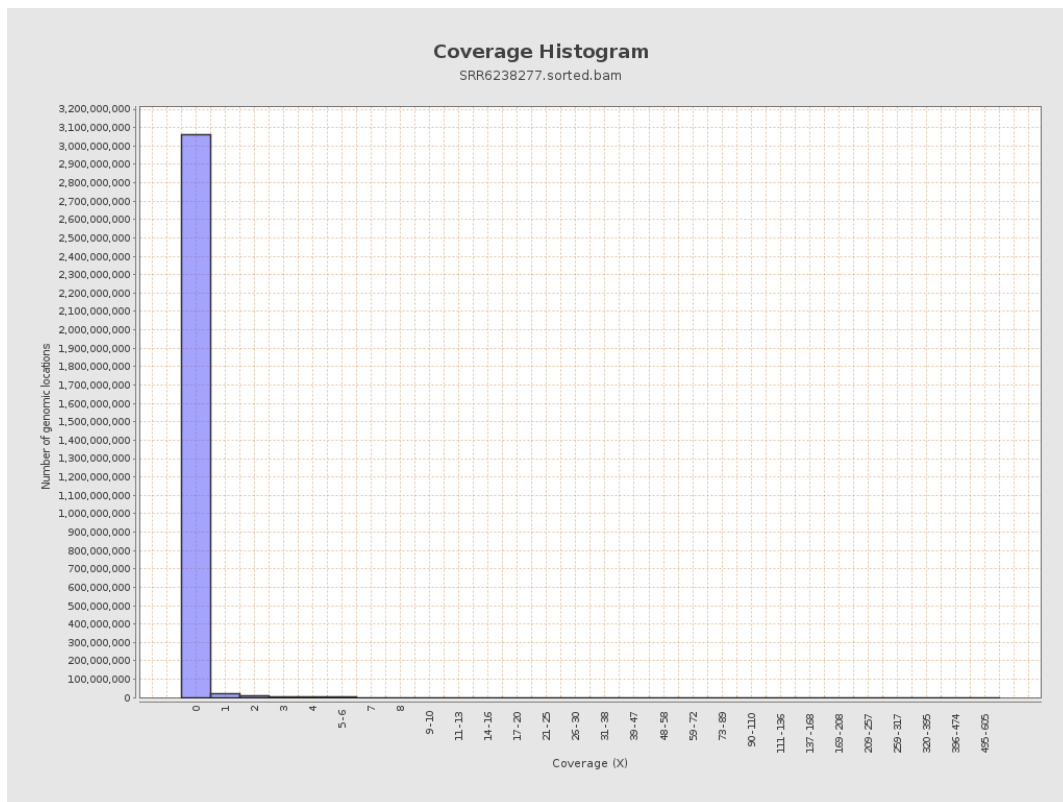
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5082852	0.0204	0.3959
chr2	243199373	5715017	0.0235	0.3818
chr3	198022430	4707841	0.0238	0.2673
chr4	191154276	4389093	0.023	0.2865
chr5	180915260	4564034	0.0252	0.2754
chr6	171115067	4026176	0.0235	0.3044
chr7	159138663	4118866	0.0259	0.3392

chr8	146364022	3496702	0.0239	0.3382
chr9	141213431	2765439	0.0196	0.2685
chr10	135534747	2915551	0.0215	0.2795
chr11	135006516	3403160	0.0252	0.2944
chr12	133851895	3312804	0.0247	0.2766
chr13	115169878	2470341	0.0214	0.2672
chr14	107349540	2378547	0.0222	0.3807
chr15	102531392	1894752	0.0185	0.4217
chr16	90354753	2044043	0.0226	0.2611
chr17	81195210	1708027	0.021	0.2537
chr18	78077248	1841929	0.0236	0.3782
chr19	59128983	1315099	0.0222	0.3202
chr20	63025520	1448964	0.023	0.2659
chr21	48129895	920814	0.0191	0.2398
chr22	51304566	801468	0.0156	0.2075
chrMT	16571	14716	0.8881	1.908
chrX	155270560	3704956	0.0239	0.2892
chrY	59373566	174912	0.0029	0.1074

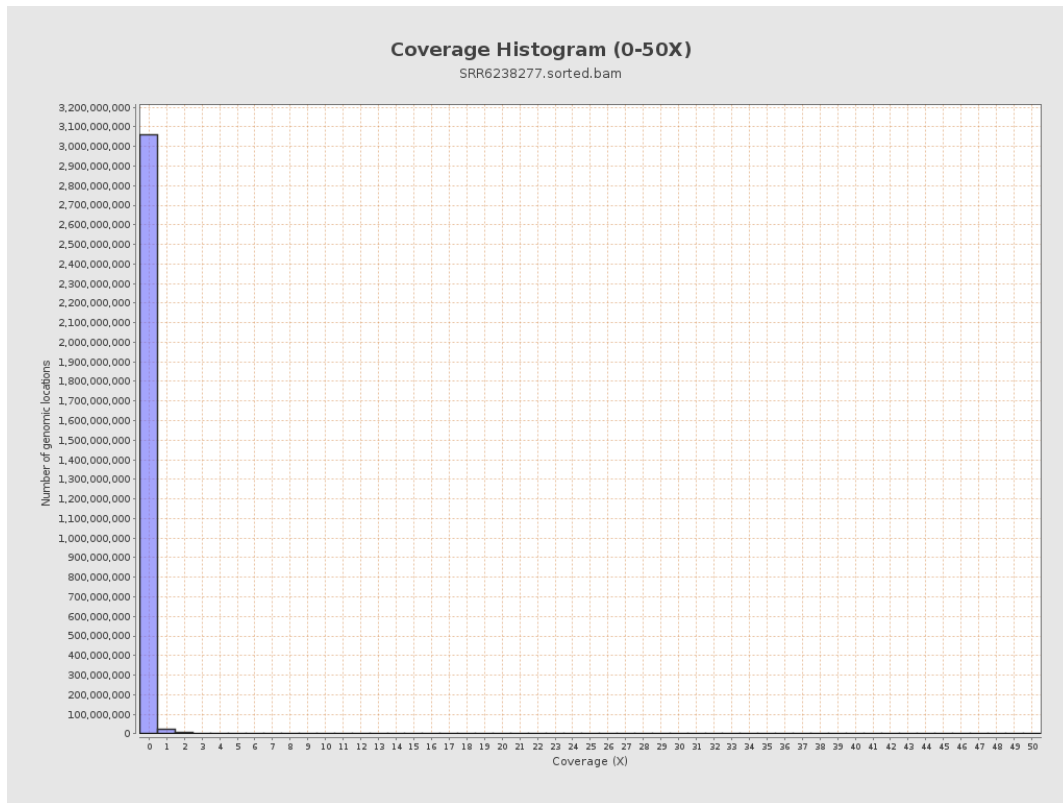
3. Results : Coverage across reference



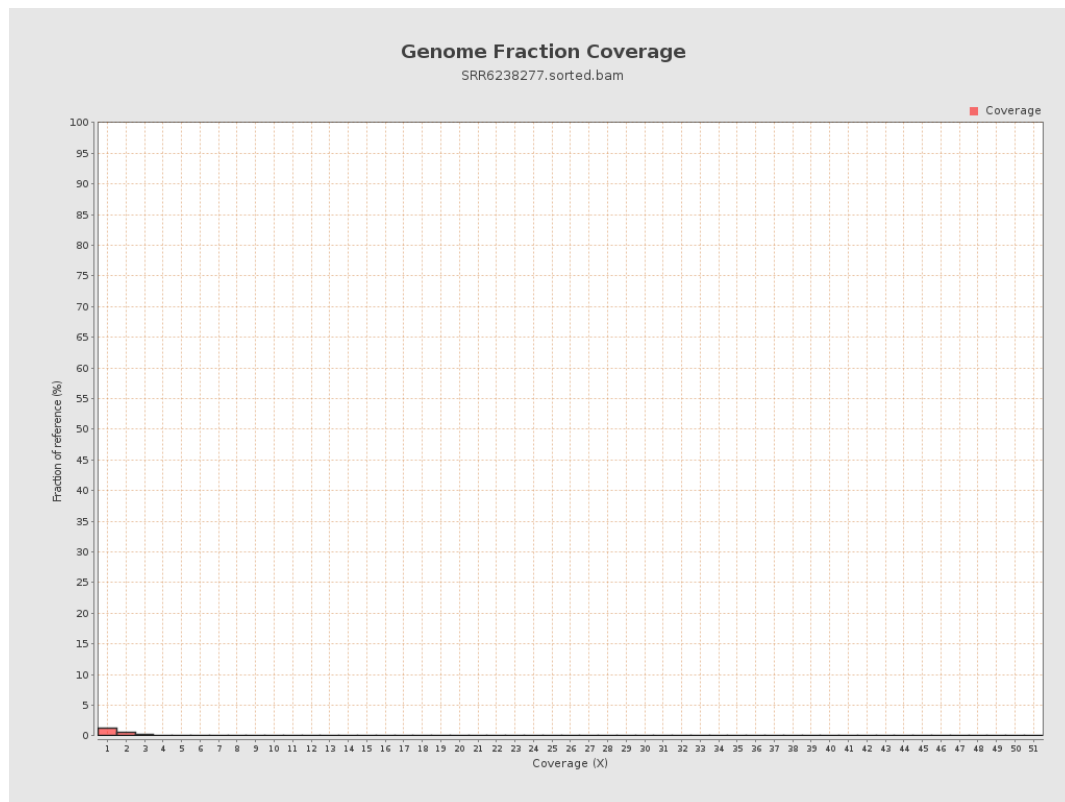
4. Results : Coverage Histogram



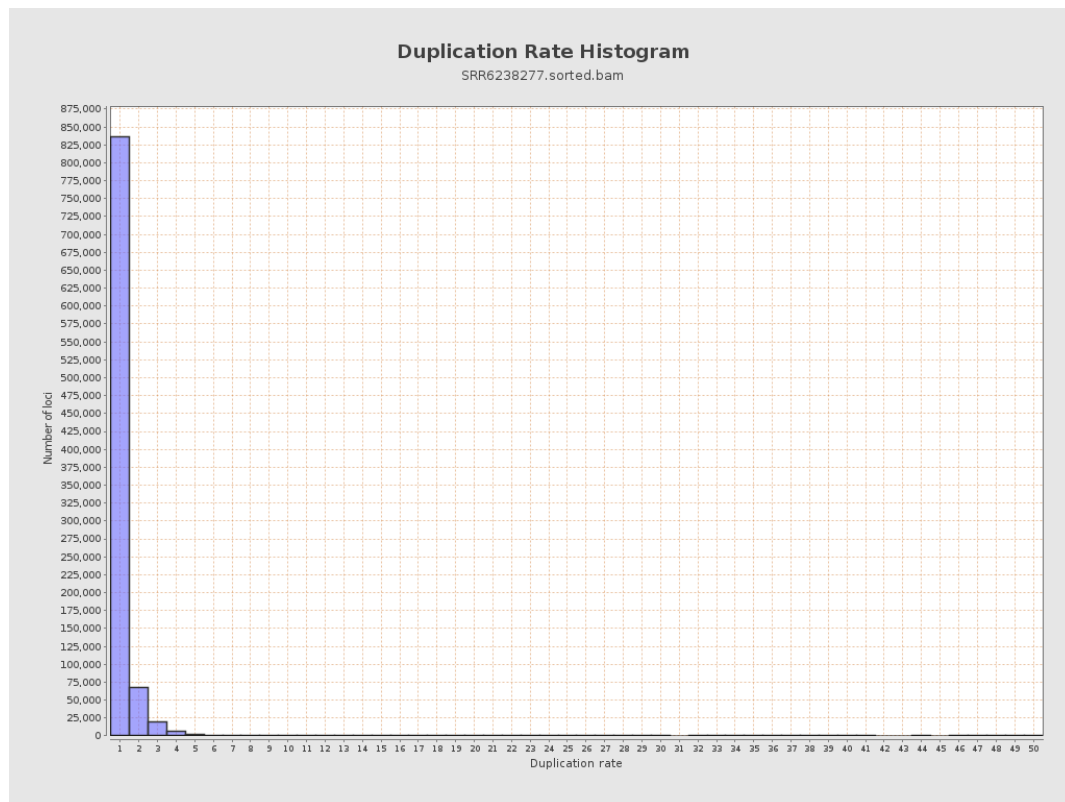
5. Results : Coverage Histogram (0-50X)



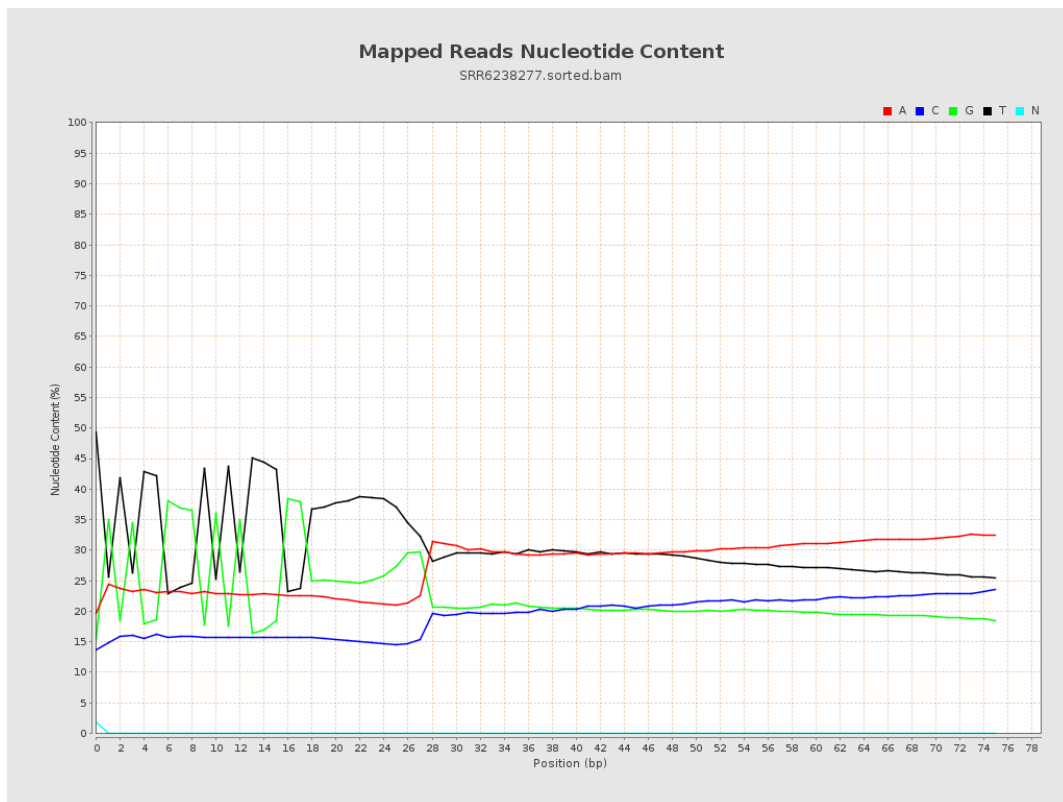
6. Results : Genome Fraction Coverage



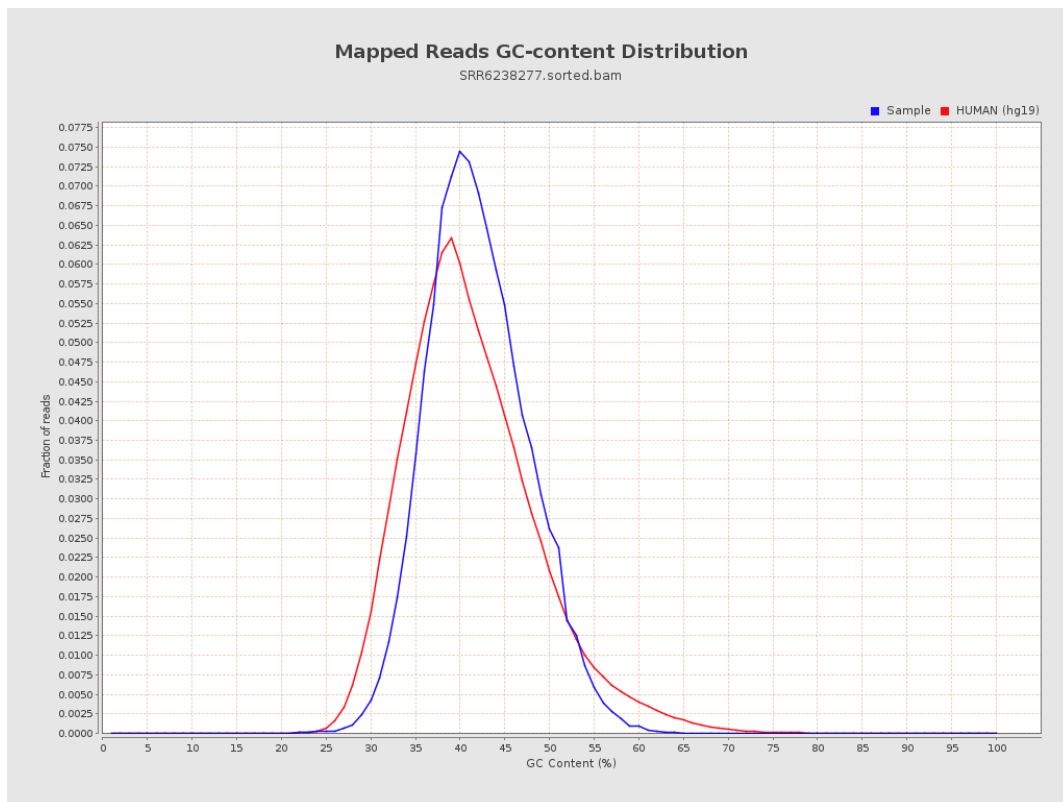
7. Results : Duplication Rate Histogram



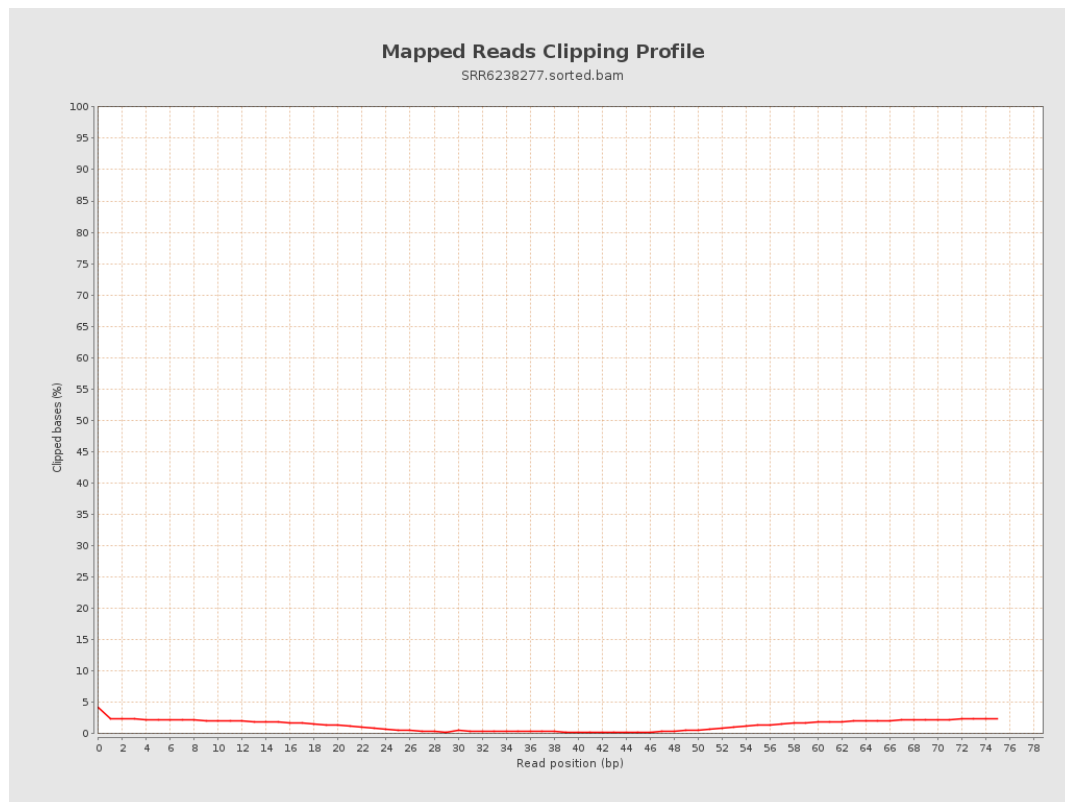
8. Results : Mapped Reads Nucleotide Content



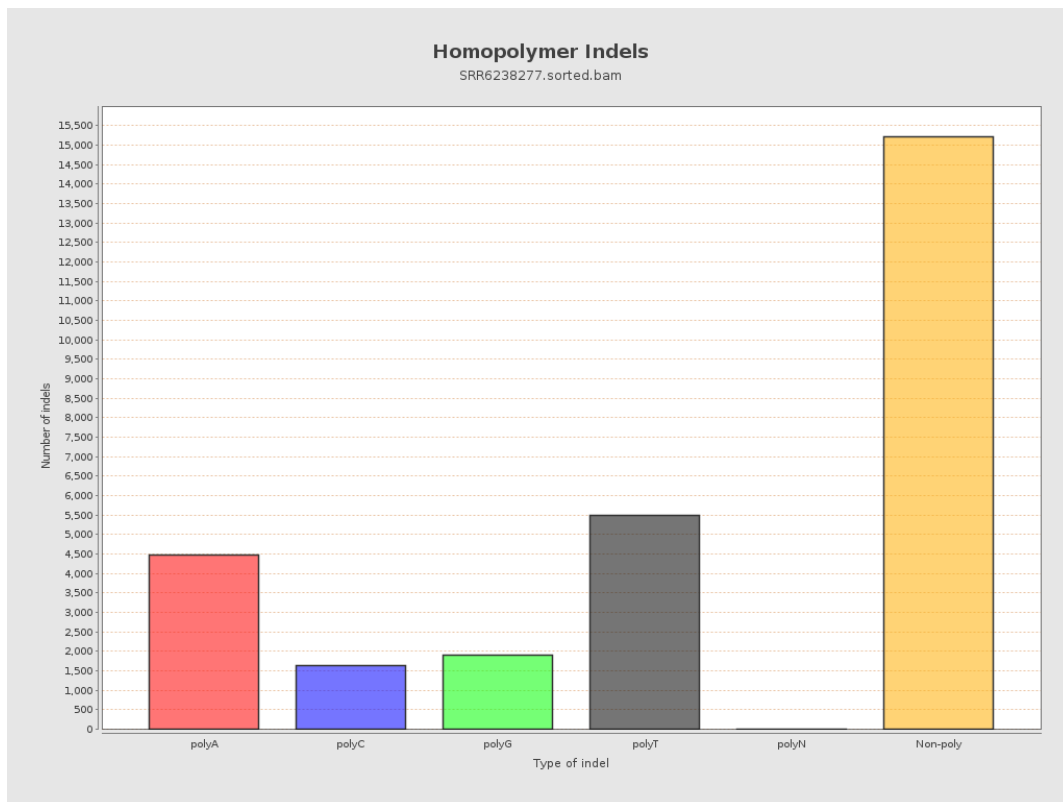
9. Results : Mapped Reads GC-content Distribution



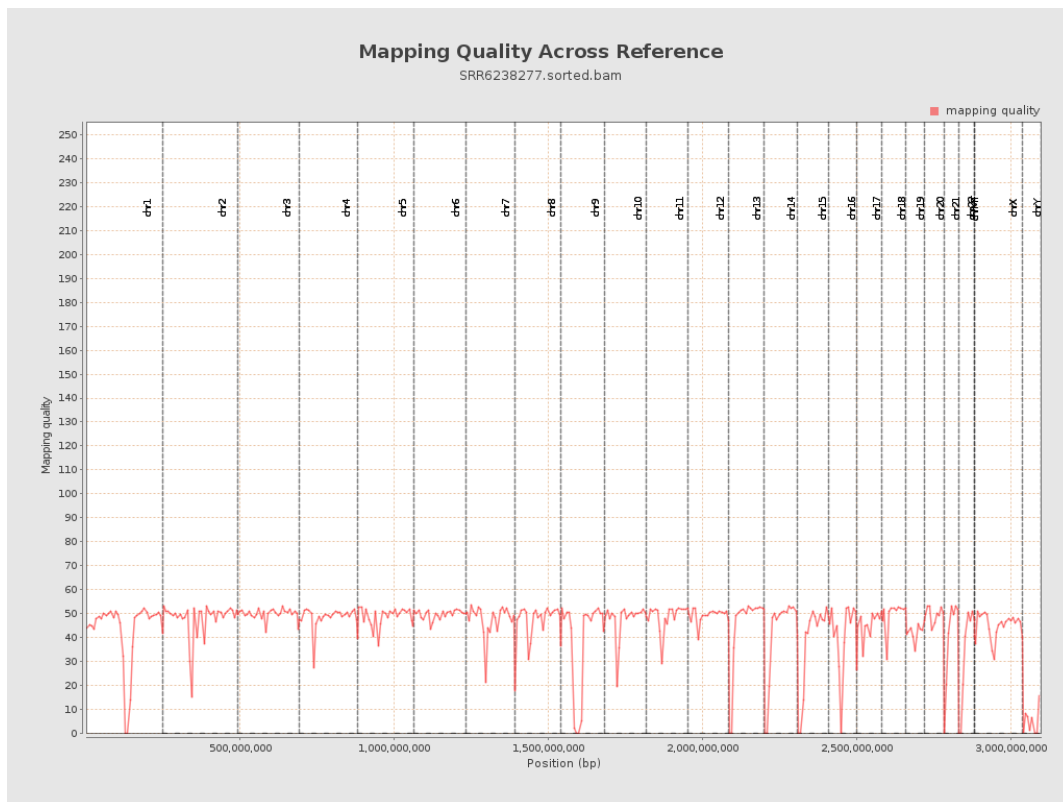
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

